DNA sequence:

caaageettgeacatgttgaegtgaacaceaaactaacaegtgteataetgeeagtggttatgataaatgeteataeeat aacaaaatgtttatattagcaaagccgccaaagtgtaaacgaaagtttataaatttcatttctgtgatcttacgtaattg gaggaagatcaaaattttcaatccccattcttcgattgcttcaattgaagtttctccg

[transit peptide start]

ATGGCGCAAGTTAGCAGAATCTGCAATGGTGTGCAGAACCCATCTCTTATCTCCAATCTCTCGAAATCCAGTCAACGCAA ATCTCCCTTATCGGTTTCTCTGAAGACGCAGCAGCATCCACGAGCTTATCCGATTTCGTCGTCGTGGGGATTGAAGAAGA GTGGGATGACGTTAATTGGCTCTGAGCTTCGTCCTCTTAAGGTCATGTCTTCTGTTTCCACGGCGGAG

[mature peptide starts]

AAAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTCTTATTAAGCTTCCTGGCTCCAAGTCTCTATCAAA  ${\tt AAAGATTGATACCATTTTGCTGTGGTTTTATAGGGAACAACTGTAGTGGACAACTTGTTGAATAGCGATGACATC}$ ATGTGGCGGGATATTCCCAGCTTCCATAGATTCAAAGAGTGATATCGAACTTTACCTCGGTAATGCAGGAACAGCAATGC GTCCACTTACCGCTGCGGTCACTGCTGCAGGTGGAAACGCAAGGTAGATTGAAGGAGTTGATGCTTCTTGGTATTTGATG TTTAAGGAATGGAGCTTTTGTTGATGCTTTATGATCCATTTATTCCAGTTATGTGCTTGATGGGGTGCCTCGTATGAGAG  $\verb|CCTGTTCGTGTCAACGCTAATGGTGGCCTTCCCGGTGGAAAGGTTAGATCTTGCAAATGGCATGTGAATATGTAATCTCG|$  $\tt TTCCTTACTCTATGAACACTTGCAGAAATGTGTGTTCATCATAGCCTTAGCTTGACAAGATTTCAGTTTTTAATCTACTC$ TCAACGGATGGATCCTAAAATAGAATCGGATTTGGTGATTGGTTTTCGTTCTCGATTACCGTTTTCGTTGTATGATTTCT TGATTAACAATTAGGAGACATGTTATGCATTTGCAGGTGAAGCTTTCTGGATCAATTAGTAGTCAGTACTTGACTGCTCT TGACATTGAAGTTGATGGAACGTTTCGGGGTTAGTGTCGAGCATAGTGATAGCTGGGATCGTTTCTTTGTCAAGGGCCCC CAAAAATACAAGTAGGAGTTATTCTTTCTTCCTTTTCTGAAATCACATCCCTTAGCTTGACAATATAATGACTAAAAGG TGAATGATTCAGGTCTCCGGGTAATGCGTATGTAGAAGGTGATGCTTCTAGTGCATGTTATTTCTTGGCTGGTGCCA GCTGTTAAGTTATAGTGAAATTCGTCTAGGTCAAAGTTTCATCTTTTGACAAGTTGTATATAACATATTCGCAAGATTC TAAGCTCAATTTTTGTGATGAATCTCTAGGGAGATGTAAAATTCGCCGAGGTCCTTGAGAAAATGGGATGTAAAGTGTCC TGGACAGAGACAGTGTGACTGTGACAGGACCACCTAGAGATGCTTTTGGAATGAGACACTTGCGGGCTATTGATGTCAA CATGAACAAAATGCCTGATGTAGCCATGACCCTTGCCGTCGTTGCTCTTTTGCTGACGGTCCAACCACCATTAGAGATG  $\tt GTAAGTAAAAAGCTCTCTCTTATAATTAAGGTTTCTCAATATTCATGATCACTTAATTCTGTTTGGTTAATATAGTGGCT$  $\verb|TTCTGTCTTGACAGTGCTCATTCTAAGTAATTAGCTCATAAATTTGTGTGTTTGTGTTCAGCTGGGAGCTACAGTGGA|$ AGAAGGTTCAGATTATTGTGTGATAACTCCGCCCAAAAAGGTGAAAACGGCAGAGATTGATACATATGATGATCATAGAA  $\tt TGGCAATGGCATTCTCTCTTGCAGCTTGTGCTGATGTTCCAATCACCATCAACGACTCTGGTTGCACCAGGAAAACCTTC$ CCCGACTACTTCCAAGTACTTGAAAGAATCACAAAGCACTAAacaataaactctgttttttcttctgatccaagctt

FIG 1A

MAQVSRICNGVQNPSLISNLSKSSQRKSPLSVSLKTQQHPRAYPISSSWGLKKSGMTLIGSELRPLKVMSSVSTAE KASEIVLQPIREISGLIKLPGSKSLSNRILLLAALSEGTTVVDNLLNSDDINYMLDALKRLGLNVETDSENNRAVV EGCGGIFPASIDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYVLDGVPRMRERPIGDLVVGLKQLGADVECTLG TNCPPVRVNANGGLPGGKVKLSGSISSQYLTALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSVEHSD SWDRFFVKGGQKYKSPGNAYVEGDASSACYFLAGAAITGETVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTENSV TVTGPPRDAFGMRHLRAIDVNMNKMPDVAMTLAVVALFADGPTTIRDVASWRVKETERMIAICTELRKLGATVEEG SDYCVITPPKKVKTAEIDTYDDHRMAMAFSLAACADVPITINDSGCTRKTFPDYFQVLERITKH

FIG. 1B

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	<u> Arabi</u>	dopsis	thalia	ina m	utant	seque	nces:				
Name A <sub>177</sub>	CTC L	GGT 1 G	N AAT C	SCA (	GCA F	ACA C	GCA A A	TG C M	R R	CCA C P	CTT L
I <sub>178</sub>	CTC L	GGT I	O TAA N	GCA (	GGA Z	ATA (	GCA A	ATG C M	CGT ( R	CCA (	CTT L
A <sub>177</sub> I <sub>178</sub>	CTC L	GGT G	) TAA N	GCA A	GCA . A	ATA I	GCA A	ATG C M	CGT ( R	CCA P	CTT L
I <sub>178</sub> S <sub>182</sub>	CTC L	GGT G	TAA N	GCA A	GGA G	ATA I	GCA A	ATG (	CGT R	TCA S	CTT $L$
$A_{177}S_{182}$	CTC L	GGT G	AAT N	GCA A	GCA A	ACA T	GCA A	ATG M	CGT R	TCA S	CTT L
A <sub>177</sub> I <sub>178</sub> S <sub>182</sub>	CTC	GGT G	TAA N	GCA A	GCA A	ATA I	GCA A	ATG M	CGT R	TCA S	CTT L
$V_{178}S_{182}$	CTC	GGT		GCA A	GGA G	GTA V	GCA A	ATG M	CGT R	TCA S	CTT L
$ m L_{178}S_{182}$	CT( L	GGT		GCA A	. GGA <i>G</i>	TTA	GCA A	ATG M	CGT R	TCA S	CTT L
A <sub>177</sub> V <sub>178</sub>	CTO	G GGT	TAA '	GCA A	GCA A	GTA V	GCA A	ATG M	CGT R	CCA P	CTT L
$\mathbf{A}_{177}\mathbf{L}_{176}$	CT	( (RFI	raa t	n GCA A	∖ GCA A	A TTA	GCA A	. ATG M	CGI R	CCF	T,

FIG. 2

petaroacDNA.SEQ GANAAATTCAGCAAATT-----CTATGTTTGGTTTTGAAAAAAGATTCAATTT-----TATGCAAAAGTTTTG petaroacdaa.seq TUTOTICIOCACACADAMAGOGICGGAGATIGIACTICAACCCATTAGAGAAATCICCGGGTCTIATTAAGCTTCCTGGC atepspscdna.seQ SCASCATCCACGAGCTTATCCGATTTCGTCGTGGGGGATTGAAGAAGAGGTGGGGATGACGTTAATTGGCTCTGAGCTTCG atepspscDNA.SEQ GGOTCAAGGGATACAAACCOTTA---ATCCCAAGTCCAAATTCCATAAACCCCAAGTTCCTAAATCTTCAAGTTTTCTTG DELAKOACDMA.SEQ CONSIDERCONGNACCOAT -- CTCTTATCTCCAATCTCTCGAAATCCAGTCAACGCAAATCTCC---CTTATCGG atepspscDNA.SEQ TOTICTICTICACGTCCGAGAAAGCTTCAGAGATTGTGCTTCAAATCAGAAATCTCGGGTCTCATTAAGCTAGCGGA bnopscDNA.SEQ -----AGATOGTGGTGGAGGCCJATCANGGAGATCTQGGGCACCGTCAAGGTGCGGGG zmepsps.SEQ ----- Zmepsps.SEQ (TONGTEGOTACACACACACACATORICATICAACAACCCATTAAAGAGATTTCAGGCACTGTTAAATTGCTGGC 90 270 170 260 160 240 140

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	TEGGACTRADIGESGAAACTGACAAATAATCGTGCTGTAGTTGAAGGATGTGGCGGGATATTCCCAGCTTCATAGA atepspscDNA.SEQ TCGGGCTTAACGTGGAACGTGACAACATGTAAACAACGTGCGGTGAAGGATGCGGTGGAATATTCCCAACTTGCTTAAGA bnepscDNA.SEQ TTGGGCTTAACGTGGAAGAAGAAACGAACGAAGGTGTTGATGAAGGTTGTGGTGGTGGTGGTGTTCCCAGTTGCTAAAGA petaroacDNA.SEQ TTGGAACTGCATGTAGAAGAAAGAAGGTGCAAAAGAGGTGTTGTTGGTGGTGGTGGTGGAAAGTTCCCAGTTGAGGA zmopsps.SEQ	
490	TCCTTAGA TCCTTAGA TGCTAAGA TGAGGA	
480	Triccaect Triccaect Triccaect	
470	rggcgggath rggrggggt rggrggggt rggrggaaa	
460	ngaaggarg ngaaggarg ngaaggric ngricgcrg	
450	GTGCTGTAGT GTGCGGTTGT GAGCTGTTGT GAGCTGTAGT	
440	TANATARTO TANACARCO SCADACCARA SCTCCCARAN	
430	ACTGACAGTC CGTGACAGTC GAAGATAGTC	
1000	TEGGACTTAATGEGGAAACTGACAAATAATAATCGTGCTGTTGTTGAAGGATGTGGCGGATATTCCCAGCTTCCTTAGA ALEPSPSCDNA.SEQ TCGGGCTTAACGTGGAAACTGACAGTGTTAAACAACGGGGTTGTTGAAGGATGCGGTGGTGGAATATTCCCAGGTTCCTTAAGA bnepscDNA.SEQ TTGGAGCTGCATGTAGAAGAAAAAAACAAACGAACGAGGTGTTGTTGAAGGTTGTTGGTGGTGGAAAGTTCCCAGTTGCTAAAGA petaxoacDNA.S	
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	SECONDARY SECAGGAACAGCAATGCGACTTACCGCTGCGGTCACTGCTGCAGGGGGAACGCAAGTTATGTA ALEPSPSCDNA.SEQ	GTTGTACCTTGGCAATGCAGGAACAGCCATGCGTCCACGCGTGCAGGCTACAGTGCTGGAAATTCAAGGTATGTA petaroacDNA.SBQ	sps.SEQ	
	atep bneb	, pete	zmer	
270	TTATCTS	SCTATGIA	TTTACGTG	
580	SAAACGCAAC	SNAATTCAAC	GANATIGCNAC	
570	CTGCAGGTG	CICACCIC TAGCTCGTG	SCTCCTCCTC	
260	GCGGTCACTG	GCAGTTACAG	CTTO THE TOTAL	
550	ACTIACCOCT	ACTCACCCCT	ACIMACAGO?	
540	AATGCGTCC	CATCCGTCC	CAATGCGGCC	CAMINCGGCC
530	CAGGAACAGG	CAGGAACAG	CAGGRACAGO	CTGGAACTG
, , , , , , , , , , , , , , , , , , ,	SERVE SECTION OF SECTI	ACCTTGGGAATG	JOUGHANTSCANATSCASSANGASCASCANTSCASCUCALINACASCASCASCASCASCASCASCASCANATISCANATISCANATISCASCANATISCASCANATI	CITTGGGGAATG
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FIG. 3A

CCANGAGTUT CCANGGAA

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CADAMACY

690  CTAACT atepspscDNA.SEQ  CTAACT bnepscDNA.SEQ  CGAAN' petaroacDNA.SEQ  CTGACT zmepsps.SEQ	790 ICATGTC atepspscDNA.SEQ ICATGC bncpscDNA.SEQ ITATGGC petaroacDNA.SEQ IGATGGC zmepsps.SEQ	890  TTTCGGG atepspscDNA.SEQ  TTTTCGGT bnepscDNA.SEQ  MTTTGGGT petaroacDNA.SEQ  MTTTGGT zmepsps.SEQ	990 rgcTTCTA atepspscDNA.SEQ rgcTTCTA bnepscDNA.SEQ rgcTTCAA petaroscDNA.SEQ rgcCTCAA znepsps.SEQ	1090 ATTCGCCGA atcpspscDNA.SEQ ATTTGCTGA bnepscDNA.SEQ ATTTGCTGA petaroacDNA.SEQ GTTTGCTCA zmepsps.SEQ	1190  TTGCGGGCT atepspscDNA.SEQ  TTGCGTGCT bnepscDNA.SEQ  TTGCGTGCC petaroacDNA.SEQ  CTGCAAGGCC zmepsps.SEQ
670 680 TGATGTTGAATGTTACTTGGAATGTTGGTACTTGGGAATGTTGGTACTTGGGTACTTGGTACTTGGTACTTGGTACTTGGTACTTGGTACTTGGTACTTGGTACTTGGGAATGTTTGTT	TAGUCAGIACTGACTGCTCTGC TAGUCAGIACTTGACTGCCTCC TAGTCAGTACTTGACTGCTGTGC CAGTCAGTACTTGAGTGCCTTGC	880 NTGACATTGAAGITTGATGGAAG NTGACATTGAAGTTGATGGAGG	0 970 980 GCTAANGGGTATGTAGAAGGTGF GGTAATGGTTATGTAGAAGGTGF GGAAAAGGCTTTTGTGTGAAGGTGG	1060 1070 1080  TACCAGCTTGCAGGAGATGTAAA CAACTAGCTCCAGGGAGATGTGAA CAAACAGTTTACAGGGGATGTGAA CCACCAGTTTACAGGGGATGTGAA	1160 1170 1180 ragagargertringgaargaggagagagagagagagagagagagagagagag
640 650 660 TGTTGGTCTTAAGCAGCTTGGTGG TGATGGTCTTAAAGAGCTTGGTGC TGATGGATTGAAGCAGCTTGGTGC	Creangertrengarearragistrenarragistrenarragistrenarrengarecateragistrenarragi	840 1TAATITICTGTTCCATATGTTGAA CTGATATCTGTTCCATATGTTGAA CTGATTAGTGTACCTTATGTCGAGA TTAATCTCCATTCCGTACGTCGAA	940 950 960 36CGGGCAAAATACAAGTGGCCTG 36AGGTCAGAAATACAAGTCTCTG 36AGGTCAAAAATACAAGTCCCTG	1030 1040 1050 1060 1060 1070 1080 1090 GGGAAAATGTAAAATTCGCCGAAGTGAAAATTCGCCGAAGTGAAAATTCGCCGAAGTGAAAATTCGCCGAAGTGAAAATTCGCCGAAGTGAAAATTCGCAAGTGAAAATTCGCAAGTTAAAAAAAA	1140 1150 1 grereacrereacheerecere erereacrereacreeacerech erereacaereanagaeerech erereacaerenagaeerech
620 670 680 690 690 690 690 690 690 690 690 690 69	720 770 780 790 790 790 790 790 790 790 790 790 79	850 860 870 890 890 890 890 890 890 890 890 890 89	PONTICIONA ANTICIONA DE 10 950 960 970 980 990 990 990 990 990 990 990 990 99	SCREET CONTROLLE TO SO TO SO TO SO SON SON SON SON SON SON SON SON SON	1190 1190 1190 1190 1190 1190 1190 1190
600 CTT STEGGGT CTT CANGE CTT CATGGGGT CTT CANGE CTT CATGGGGT CTT CANGE	17.	BOO DESCRIPTION OF THE PROPERTY OF THE PROPERT		100 100 100 100ATWITE 100ATWITE 100ATWITE 100ATWITE 100ATWITE	64 CYCONGCOT CALLS 1110 105. CYCCOTTGACT GGAN 106. CYTCOTTGACT GGA

FIG. 3B

atopspscDNA.SEQ bnepscUNA.SEQ petaroacDNA.SEQ zmepsps.SEQ	atepspscDNA.SEQ bnepscDNA.SEQ petaroacDNA.SEQ zmepsps.SEQ	atepspscDNA.SEQ bnepscDNA.SEQ petaroacDNA.SEQ zmcpsps.SEQ	atepspscDNA.SEQ bnepscDNA.SEQ petaroacDNA.SEQ zmepsps.SEQ
1250 1230 1230 1230 1240 1250 1260 1270 1280 1290 1290 1290 1290 1290 1290 1290 129	1320 1390 1390 130 1340 1350 1360 1370 1380 1390 1390 AANSSATGATTGCCATTTGCACAGAGCTTAGAAAACTGGAAGCTACAGATCAGATTGTGTGATAACTCC ALEBSPSCDMA.SEQ AGAGGATGATTGCCATTTGCACAGAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGCTTAGAAGAAGAAGAAGAACTTAGAAGAAGAAGAAAGA	1420 1490 1490 1490 1450 1460 1470 1470 1490 1490 SECONDA.SEQ SECONDARIONALINA SECONDARIONAL SEQ SECONDARIONAL SEQUENCIA SEQUENCIA SEQUENCIA SEQUENCIA SEQUENCIA SEQUENCIA SEQUENCIA SEQUENCIA SE SECONDARIONAL SEQUENCIA SEQUEN	1520 1520 1530 1540 1550 1560  AGGAAAAGCTTCCCCGACTACTTCAAAGAATCACAAAGCACTAA CAGGAAAACTTTCCCTGAAGTCCTTCAAAGTATCACAAAGCATTAA SCGGAAAAACTTTCCCTGAAGTCTTCAAAGTATCACAAAGCATTCAAAAGTATTCAAAAGTATTCAAAAAAAA
120. 2 A DESTATORANDO DESTANDA DESTAND	130 	140: 92	1.50 1.92 NACGACTOTAL 1.80 NACGATOOTÄG 1.80 NATGATOOTÄG

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100 LOLIKLPGSKSLSN GLIKLPGSKSLSN GTVKLPGSKSLSN	200 210 DGVPRMRBRPICDLV DGVPRMRBRPIGDLV DGVPRMRBRPISDLV DGVPRMRBRPIGDLV	310 DEVKGGQKYKSPGNA PRVKGGQKYKSPGNA PRVKGGQKYKSPGKA	420 ADGPTTIRDVASWRV ADGPTTIRDVASWRV ADGPTATRDVASWRV	
AYPISSSWGIRKSGATLIGSELRPLKVMSSVSTAEKASEIVLQPIREISGLIKLPGSKSLSN PRASSWGLKKSGTMLNGSVIRPVKVTASVSTSRKASEIVLQPIREISGLIKLPGSKSLSN LKNSANSMLVKKDSIFWQKFCSFRISASVATÄQKPSEIVLQPIKEISGTVKLPGSKSLSN	170 180 190 200 210  ASDDINYALDALKRIGLAW ETDSENNRAVVEGCGGIFFASIDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYVLDGVPRARBRPIGDLW ALEDSDS.PRO ASDDINYALDALKRIGLAW ETDSENNRAVVEGCGGIFFASIDSKSDIELYLGNAGTAMRPLTAAVTVAGGNASYVLDGVPRARBRPIGDLW bnepsps.PRO ASSDDIHYMIGALKTIGLHVEEDSANQRAVVEGCGGLFPVGKESKEETQIFLGNAGTAMRPLTAAVTVAGGNSRYVLDGVPRARBRPISDLW zmepsps.PRO ASEDVHYMIGALRTIGLSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFIGNAGTAMRPLTAAVTAAGGNATYVLDGVPRARBRPIGDLW zmepsps.PRO	240 250 310 320 320 290 300 310 320 320 290 300 310 320 2PVRVNRANIAMENEGYSVEHSDSWORFFVKGGOKYKSPGNA PYRVNANGGLPGCKVKLSGSISSQYLTALLMSAPLALGDVEIEIIDKLISVPYVENTLKLMERFGVSVEHSDSWORFFVKGGOKYKSPGNA PYRVNANGGLPGCKVKLSGSISSQYLTALLMAAPLALGDVEIEIIDKLISVPYVENTLKLMERFGVSVEHSSSWORFFVKGGOKYKSPKNA PVVRVNGIGGLPGCKVKLSGSISSQYLTALLMAAFLALGDVEIEIIDKLISIPYVENTLKLMERFGYKABHISDSWORFYIKGGOKYKSPKNA PVVRVNGIGGLPGCKVKLSGSISSQYLSALLMAAFLALGDVEIEIIDKLISIPYVENTLRLMERFGYKABHISDSWORFYIKGGOKYKSPKNA	350 360 370 380 390 400 410 420 430  GETVTVBGCGTTSLQGDVKFAEVLEKMGCKVSWTENSVTVTGPPRDAFGMRHLRALDVNMANKNIPDVAMTLAVVALFADGPTTIRDVASWRV TGETVTVFGCGTTSLQGDVKFAEVLEKMGCKVSWTENSVTVTGPPRDAFGMRHERAVDVNMANKNIPDVAMTLAVVALFADGPTTIRDVASWRV TGSTTTVFGCGTTSLQGDVKFAEVLEKMGAEVTWTENSVTVTVGPPRSSSGRKHLRALDVANMANKNIPDVAMTLAVVALFADGPTAIRDVASWRV	S20 SRITKH SSITKH SUFSKH STFVKN
70 10 PLKVMSSVSTAE PVKVTASVSTSE FCSFRISASVATÄG	180 LGNAGTAMRPLTA TLGNAGTAMRPLTA TLGNAGTAMRPLTA	290 SVPYVEMTLKLMER SVPYVEMTLKLMER SVPYVEMTLKLMER SI PYVEMTLRLMER	400 MRHLRAIDVNMWKN MRHLRAVDVNMWKN RKHLRAIDVNMWKN	460 470 480 490 500 510 520 520 520 520 520 520 520 520 520 52
60 SMTLIGSELR STMLNGSVIR	160 170 PASIDSKSDIELY FPASLDSKSDIELY FPASLDSKSDIELY FPVGKESKEELQE	270 280 LGDVELEIVDKLI LGDVELEIJDKLI LGDVELEIJDKLI	380 390 RVIVIGPPRDAFG RVIVIGPPRSSSG RSVIVIGPPRESSG	A90 500 AACADVPITINDSGAACADVPVTINDPC
26 50 66 66 66 74.2.SKSSQRKSPLSVSLKTQQHPRAYPISSSWGLKKSGMTLIGSELR	150 ENNRAVVEGCGGI VNNRAVVEGCGGI ANGRAVVGCGGK	260 COYLTALLMSAPLA QYLTALLMAAPLA SQYLTALLMAAFLA SQYLSALLMAAFLA	370 TLEKMGCKVSWTEN TLEKMGCKVSWTEN TLEKMGAEVTWTEN	180 LISAMANAFISIA LISDOHRMANAFISIA LISDOHRMANAFISIA LISDOHRMANAFISIA
26 30 40 NESKSSQRKSPLSVSLKTQQHPPUNTGKSIQNKSPFSVSLKTHQNFHKPQVPKSSSFLVFGSKK	130 140 NSDDINYMIDALKRUGLAVETDS NSDDINYMIDALKRUGLAVERDS SSDDINYMIGALKTUGLAVEEDS NSEDVHYMLGALRTLGLSVEADK	240 250 PVRVNANGGLPGCKVKLSGSISS PVRVNANGGLPGCKVKLSGSISS PVRVNGGGLPGCKVKLSGSISS	360 GTTSLQGDVKFAEK GTTSLQGDVKFAEK GTTSLQGDVKFAEK	460 470  WEEGSDYCVITPPRKVKTAELD  WEEGSDYCVITPPAKVKPAELD  WEEGPDYCITPPEKLAVTBID
26 NESKSSQRWS NESKSSQRWS NESKSRQVPKS	DEL THMANICOSSI THMANICOSSI DE	240 PVRVNANGG PPVRVNANGG PVRVNANGGG	1 250 250 250 250 250 250 250 250 250 250	460 TVBEGSDYCV TVBEGEDYCY TVBEGEDYCI
10 MALOSRICHOVOS MAQSSRICHOVOS MALOSRICHOVOS MALOSRICHOVOS	110 210 3 ETTLANISEGT 5 ETTLANISEGT 7 ETTLANISEGT 7 ETTLANISEGT	220 220 14 1.1X2DGADVB 10 1.1X2DGADVB 10 1.1X2DGABVB 19 1.1X2DGABVB	330 24 VUSGDASSACVI 20 VUGDASSASVI 20 VUGDASSASVI 18 VUGDASSASVI	440 194 ESTERMIAICA. 190 VERRINIAICA. 180 VERRINIAICA.



## Oligo Name Oligo Sequence (5'→3')

ATEPS-A <sub>177</sub>
CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGGACGCATTGCTGTTGCTGCATTACCGAG
ATEPS-AI
CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGGACGCATTGCTATTGCTGCATTACCGAG
ATEPS-IS
CGITTCCACCIGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTATTCCTGCATTACCGAG
ATEPS-AS
CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTGTTGCTGCATTACCGAG
ATEPS-AIS
OGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTATTGCTGCATTACCGAG
ATEPS-I <sub>177</sub>
CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAGTGGACGCATTGCTGTTATTGCATTACCGAG
ATEPS-VS
CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTACTCCTGCATTACCGAG
ATEPS-LS
CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTAATCCTGCATTACCGAC
ATEPS-AV
CGTT1CCACCTGCAGCAGTGACCGCAGCGGTAAGTGGACGCATTGCTACTGCTGCATTACCGAC
ATEPS-AL
CONTINUE DE CONTRE DE CARTIGA CON PROPERCIONA DE LA CONTRE CONTRE CONTINUE DE CONTRE C

## FIG. 5

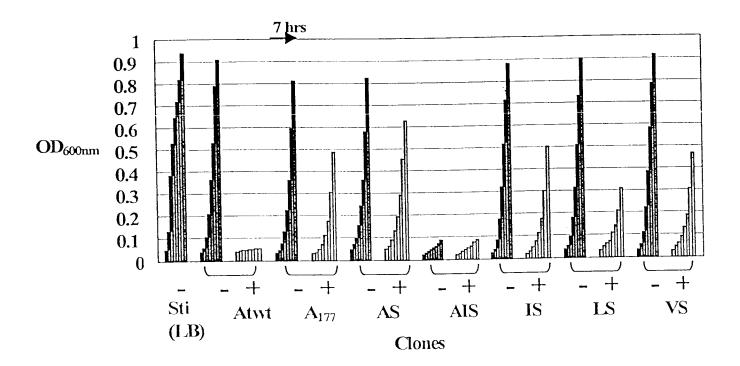
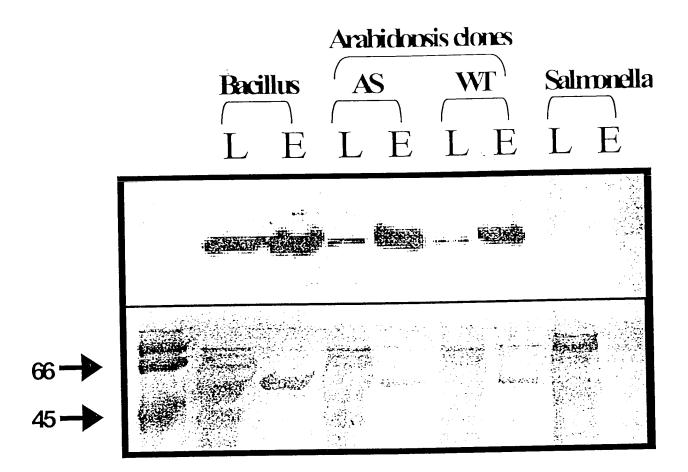


FIG. 6



**FIG.** 7